# TESTING PROTEIN STRUCTURE PREDICTION BY MEANS OF A BLIND PREDICTION PROCESS

Krzysztof Fidelis, Ceslovas Venclovas, and Adam Zemla
Protein Structure Prediction Center,
Biology and Biotechnology Research Program,
Lawrence Livermore National Laboratory, Livermore, CA 94551.
kaf@sb1.llnl.gov, venc@sb2.llnl.gov, adamz@sb9.llnl.gov
http://PredictionCenter.llnl.gov

and

John Moult
Center for Advanced Research in Biotechnology,
University of Maryland Biotechnology Institute, Rockville,
MD 20850.

Objective assessment of the methods for protein structure prediction is necessary to effectively advance their future development. We have addressed this issue by building a network based facility which provides prediction targets, accepts predictions, and makes evaluations according to a detailed set of criteria. Targets for predictions are selected from structures that are about to be released publicly. Predictions are accepted in comparative modeling, fold recognition, and ab initio folding. Livermore based center provides this service on continuing basis as well as in conjunction with the bi-annual Meeting on Critical Assessment of Techniques for Protein Structure Prediction (CASP1 1994 and CASP2 1996). We will present the details of the blind prediction process, evaluation criteria, and some of the results from the 1996 meeting.